

SEQUENCE LISTING

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<120> Genes and Proteins, and Their Use

<130> GJE-70

<140> US 09/868,352

<141> 2001-06-15

<160> 35

<170> PatentIn version 3.1

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<211> 587

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (582)

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Met Ile Pro Val Val Ile Glu Gln Thr Ser Arg Gly Glu Arg Ser Tyr	
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gat att tac tca cgt ctt tta aaa gat cgt att att atg ttg aca ggc	96
Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Ile Met Leu Thr Gly	
20 25 30	
caa gtt gag gat aat atg gcc aat agt atc att gca cag tta ttg ttt	144
Gln Val Glu Asp Asn Met Ala Asn Ser Ile Ile Ala Gln Leu Leu Phe	
35 40 45	
ctc gat gca caa gat aat aca aag gat att tac ctt tat gtc aat aca	192
Leu Asp Ala Gln Asp Asn Thr Lys Asp Ile Tyr Leu Tyr Val Asn Thr	
50 55 60	
cca ggt ggt tca gta tcg gct gga ctt gct att gtg gac acc atg aac	240
Pro Gly Gly Ser Val Ser Ala Gly Leu Ala Ile Val Asp Thr Met Asn	
65 70 75 80	
ttc att aaa tcg gac gta cag acg att gtt atg ggg atg gct gct tcg	288
Phe Ile Lys Ser Asp Val Gln Thr Ile Val Met Gly Met Ala Ala Ser	
85 90 95	
atg gga acc att att gct tca agt ggt gct aaa gga aaa cgt ttt atg	336
Met Gly Thr Ile Ile Ala Ser Ser Gly Ala Lys Gly Lys Arg Phe Met	
100 105 110	
tta ccg aat gca gaa tat atg atc cac caa cca atg ggc gga aca ggc	384
Leu Pro Asn Ala Glu Tyr Met Ile His Gln Pro Met Gly Gly Thr Gly	
115 120 125	
gga ggt aca cag caa tct gat atg gct atc gct gct gag cat ctt tta	432
Gly Gly Thr Gln Gln Ser Asp Met Ala Ile Ala Ala Glu His Leu Leu	
130 135 140	

aaa acg cgt cat act tta gaa aaa atc tta gct gat aat tct ggt caa 480
 Lys Thr Arg His Thr Leu Glu Lys Ile Leu Ala Asp Asn Ser Gly Gln
 145 150 155 160

 tct att gaa aaa gtc cat gat gat gca gag cgt gat cgt tgg atg agt 528
 Ser Ile Glu Lys Val His Asp Asp Ala Glu Arg Asp Arg Trp Met Ser
 165 170 175

 gct caa gaa aca ctt gat tat ggc ttt att gat gaa atc atg gct aat 576
 Ala Gln Glu Thr Leu Asp Tyr Gly Phe Ile Asp Glu Ile Met Ala Asn
 180 185 190

 aat gaa taagg 587
 Asn Glu

<210> 2

<211> 194

<212> PRT

<213> Streptococcus agalactiae

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 Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Ile Met Leu Thr Gly
 20 25 30

 Gln Val Glu Asp Asn Met Ala Asn Ser Ile Ile Ala Gln Leu Leu Phe
 35 40 45

 Leu Asp Ala Gln Asp Asn Thr Lys Asp Ile Tyr Leu Tyr Val Asn Thr
 50 55 60

 Pro Gly Gly Ser Val Ser Ala Gly Leu Ala Ile Val Asp Thr Met Asn
 65 70 75 80

 Phe Ile Lys Ser Asp Val Gln Thr Ile Val Met Gly Met Ala Ala Ser
 85 90 95

Met Gly Thr Ile Ile Ala Ser Ser Gly Ala Lys Gly Lys Arg Phe Met
 100 105 110

Leu Pro Asn Ala Glu Tyr Met Ile His Gln Pro Met Gly Gly Thr Gly
 115 120 125

Gly Gly Thr Gln Gln Ser Asp Met Ala Ile Ala Ala Glu His Leu Leu
 130 135 140

Lys Thr Arg His Thr Leu Glu Lys Ile Leu Ala Asp Asn Ser Gly Gln
 145 150 155 160

Ser Ile Glu Lys Val His Asp Asp Ala Glu Arg Asp Arg Trp Met Ser
 165 170 175

Ala Gln Glu Thr Leu Asp Tyr Gly Phe Ile Asp Glu Ile Met Ala Asn
 180 185 190

Asn Glu

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48

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1				5					10					15		
gct tgt gat ata ata gtc aat gtg agg agg act atc atg tta ttt aag																96
Ala	Cys	Asp	Ile	Ile	Val	Asn	Val	Arg	Arg	Thr	Ile	Met	Leu	Phe	Lys	
			20					25					30			
gaa aaa att cct gga cta ata tta tgc ttt att att gct ata cca tct																144
Glu	Lys	Ile	Pro	Gly	Leu	Ile	Leu	Cys	Phe	Ile	Ile	Ala	Ile	Pro	Ser	
		35					40					45				
tgg ttg ctt ggg ctt tat ctc cct.tta ata gga gca cca gtc ttt gct																192
Trp	Leu	Leu	Gly	Leu	Tyr	Leu	Pro	Leu	Ile	Gly	Ala	Pro	Val	Phe	Ala	
	50					55				60						
atc ttg att gga ata att gtt gga tc																218
Ile	Leu	Ile	Gly	Ile	Ile	Val	Gly									
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<213> Streptococcus agalactiae

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Ala Cys Asp Ile Ile Val Asn Val Arg Arg Thr Ile Met Leu Phe Lys																
			20					25					30			
Glu Lys Ile Pro Gly Leu Ile Leu Cys Phe Ile Ile Ala Ile Pro Ser																
		35				40					45					
Trp Leu Leu Gly Leu Tyr Leu Pro Leu Ile Gly Ala Pro Val Phe Ala																
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Ile Leu Ile Gly Ile Ile Val Gly																
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<213> Streptococcus agalactiae

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tta gct tat gga gct atc act tta gta gcc ctt ttt tca tgt att ttg	96
Leu Ala Tyr Gly Ala Ile Thr Leu Val Ala Leu Phe Ser Cys Ile Leu	
20 25 30	
gct gta acg gtc atc ttt aaa agt tca caa gtt act act gaa tct ttg	144
Ala Val Thr Val Ile Phe Lys Ser Ser Gln Val Thr Thr Glu Ser Leu	
35 40 45	
tca aaa gca gat aaa gtt cgc gta gcc aaa aaa tca aaa atg act aag	192
Ser Lys Ala Asp Lys Val Arg Val Ala Lys Lys Ser Lys Met Thr Lys	
50 55 60	
gcg aca tct aaa tca aaa gta gaa gat gta aaa cag gct cca aaa cct	240
Ala Thr Ser Lys Ser Lys Val Glu Asp Val Lys Gln Ala Pro Lys Pro	
65 70 75 80	
tct cag gca tct aat gaa gcc cca aaa tca agt tct caa tct aca gaa	288
Ser Gln Ala Ser Asn Glu Ala Pro Lys Ser Ser Ser Gln Ser Thr Glu	
85 90 95	
gct aat tct cag caa caa gtt act gcg agt gaa gag acg gct gta gaa	336
Ala Asn Ser Gln Gln Gln Val Thr Ala Ser Glu Glu Thr Ala Val Glu	
100 105 110	
caa gca gtt gta aca gaa ata ccc ctg cta cca gtc agg cac aac aac	384

Gln	Ala	Val	Val	Thr	Glu	Ile	Pro	Leu	Leu	Pro	Val	Arg	His	Asn	Asn		
		115					120					125					
ctt	tat	gct	ggt	act	gag	aca	cct	tac	aac	cct	gct	caa	cca	cca	gac	432	
Leu	Tyr	Ala	Val	Thr	Glu	Thr	Pro	Tyr	Asn	Pro	Ala	Gln	Pro	Pro	Asp		
		130				135					140						
caa	gtg	gcc	agg	tat	gag	caa	tgg	aaa	tac	tgc	cag	gcg	gtc	gga	tct	480	
Gln	Val	Ala	Arg	Tyr	Glu	Gln	Trp	Lys	Tyr	Cys	Gln	Ala	Val	Gly	Ser		
145					150					155				160			
gct	gct	gca	gca	caa	atg	gct	gct	gca	aca	gga	gtc	cct	cag	tct	act	528	
Ala	Ala	Ala	Ala	Gln	Met	Ala	Ala	Ala	Thr	Gly	Val	Pro	Gln	Ser	Thr		
				165				170						175			
tgg	gaa	cat	att	att	gcc	cgt	gaa	tca	aat	ggt	aat	cct	aat	ggt	gct	576	
Trp	Glu	His	Ile	Ile	Ala	Arg	Glu	Ser	Asn	Gly	Asn	Pro	Asn	Val	Ala		
		180					185					190					
aat	gcc	tca	gga	gct	tca	gga	ctt	ttc	caa	acg	atg	cca	ggt	tgg	ggt	624	
Asn	Ala	Ser	Gly	Ala	Ser	Gly	Leu	Phe	Gln	Thr	Met	Pro	Gly	Trp	Gly		
		195					200					205					
tca	aca	gct	aca	ggt	cag	gat	caa	gta	att	cag	cta	tta	aag	ctt	att	672	
Ser	Thr	Ala	Thr	Val	Gln	Asp	Gln	Val	Ile	Gln	Leu	Leu	Lys	Leu	Ile		
		210				215					220						
cgt	gct	caa	ggg	tta	tca	gct	ggg	tac	cag	tga						705	
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225					230												

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<212> PRT

<213> Streptococcus agalactiae

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Leu	Ala	Tyr	Gly	Ala	Ile	Thr	Leu	Val	Ala	Leu	Phe	Ser	Cys	Ile	Leu
		20					25						30		

Ala Val Thr Val Ile Phe Lys Ser Ser Gln Val Thr Thr Glu Ser Leu
 35 40 45

Ser Lys Ala Asp Lys Val Arg Val Ala Lys Lys Ser Lys Met Thr Lys
 50 55 60

Ala Thr Ser Lys Ser Lys Val Glu Asp Val Lys Gln Ala Pro Lys Pro
 65 70 75 80

Ser Gln Ala Ser Asn Glu Ala Pro Lys Ser Ser Ser Gln Ser Thr Glu
 85 90 95

Ala Asn Ser Gln Gln Gln Val Thr Ala Ser Glu Glu Thr Ala Val Glu
 100 105 110

Gln Ala Val Val Thr Glu Ile Pro Leu Leu Pro Val Arg His Asn Asn
 115 120 125

Leu Tyr Ala Val Thr Glu Thr Pro Tyr Asn Pro Ala Gln Pro Pro Asp
 130 135 140

Gln Val Ala Arg Tyr Glu Gln Trp Lys Tyr Cys Gln Ala Val Gly Ser
 145 150 155 160

Ala Ala Ala Ala Gln Met Ala Ala Ala Thr Gly Val Pro Gln Ser Thr
 165 170 175

Trp Glu His Ile Ile Ala Arg Glu Ser Asn Gly Asn Pro Asn Val Ala
 180 185 190

Asn Ala Ser Gly Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly
 195 200 205

Ser Thr Ala Thr Val Gln Asp Gln Val Ile Gln Leu Leu Lys Leu Ile
 210 215 220

Arg Ala Gln Gly Leu Ser Ala Gly Tyr Gln
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<211> 594

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<213> Streptococcus agalactiae

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<222> (1) .. (594)

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gcc att cct gaa ttg ttg gaa ttc gat att acc gtt cgt gga gac aac	96
Ala Ile Pro Glu Leu Leu Glu Phe Asp Ile Thr Val Arg Gly Asp Asn	
20 25 30	
cgt gga tgg ttc aaa gag aac ttt caa aaa gaa aaa atg ata ccg ctt	144
Arg Gly Trp Phe Lys Glu Asn Phe Gln Lys Glu Lys Met Ile Pro Leu	
35 40 45	
ggt ttc cca gaa agc ttc ttt gag gca gac aaa cta caa aat aat att	192
Gly Phe Pro Glu Ser Phe Phe Glu Ala Asp Lys Leu Gln Asn Asn Ile	
50 55 60	
tcg ttt aca aaa aaa aat act ttg cga ggt ctc cat gca gag cct tgg	240
Ser Phe Thr Lys Lys Asn Thr Leu Arg Gly Leu His Ala Glu Pro Trp	
65 70 75 80	
gat aaa tat gtt tcg atc gct gat gaa gga cgt gtg atc ggt act tgg	288
Asp Lys Tyr Val Ser Ile Ala Asp Glu Gly Arg Val Ile Gly Thr Trp	
85 90 95	
gtt gac ctc cgt gaa ggt gac agt ttt ggt aac gtt tac caa acg att	336
Val Asp Leu Arg Glu Gly Asp Ser Phe Gly Asn Val Tyr Gln Thr Ile	
100 105 110	
atc gat gcc tca aaa ggt att ttt gtt cca cgc ggc gtt gct aat ggt	384

Ile Asp Ala Ser Lys Gly Ile Phe Val Pro Arg Gly Val Ala Asn Gly	
115 120 125	
ttc caa gtt ctt tca gat aaa gca gct tat act tat ctc gtt aac gat	432
Phe Gln Val Leu Ser Asp Lys Ala Ala Tyr Thr Tyr Leu Val Asn Asp	
130 135 140	
tat tgg gca ctt gaa ctc aaa cca aaa tat gct ttc gtt aac tat gca	480
Tyr Trp Ala Leu Glu Leu Lys Pro Lys Tyr Ala Phe Val Asn Tyr Ala	
145 150 155 160	
gat cca aat cta ggc att cag tgg gaa aat ctw gaa gaa gca gaa gtc	528
Asp Pro Asn Leu Gly Ile Gln Trp Glu Asn Leu Glu Glu Ala Glu Val	
165 170 175	
tca gaa gca gat aag aat cac cca ctt ctc aaa gat gta aaa cct ttg	576
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180 185 190	
aag aag gaa gat ttg taa	594
Lys Lys Glu Asp Leu	
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<210> 8

<211> 197

<212> PRT

<213> Streptococcus agalactiae

<400> 8

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20 25 30	
Arg Gly Trp Phe Lys Glu Asn Phe Gln Lys Glu Lys Met Ile Pro Leu	
35 40 45	
Gly Phe Pro Glu Ser Phe Phe Glu Ala Asp Lys Leu Gln Asn Asn Ile	
50 55 60	

Ser Phe Thr Lys Lys Asn Thr Leu Arg Gly Leu His Ala Glu Pro Trp
65 70 75 80

Asp Lys Tyr Val Ser Ile Ala Asp Glu Gly Arg Val Ile Gly Thr Trp
85 90 95

Val Asp Leu Arg Glu Gly Asp Ser Phe Gly Asn Val Tyr Gln Thr Ile
100 105 110

Ile Asp Ala Ser Lys Gly Ile Phe Val Pro Arg Gly Val Ala Asn Gly
115 120 125

Phe Gln Val Leu Ser Asp Lys Ala Ala Tyr Thr Tyr Leu Val Asn Asp
130 135 140

Tyr Trp Ala Leu Glu Leu Lys Pro Lys Tyr Ala Phe Val Asn Tyr Ala
145 150 155 160

Asp Pro Asn Leu Gly Ile Gln Trp Glu Asn Leu Glu Glu Ala Glu Val
165 170 175

Ser Glu Ala Asp Lys Asn His Pro Leu Leu Lys Asp Val Lys Pro Leu
180 185 190

Lys Lys Glu Asp Leu
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<210> 9

<211> 1217

<212> DNA

<213> Streptococcus agalactiae

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<222> (571)..(571)

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<222> (1) .. (570)

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<222> (679) .. (945)

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<400> 9

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1				5				10					15			

tct	ttt	gat	aaa	gca	tca	aaa	gca	gga	ttt	att	att	gct	tta	ggc	att	96
Ser	Phe	Asp	Lys	Ala	Ser	Lys	Ala	Gly	Phe	Ile	Ile	Ala	Leu	Gly	Ile	
			20					25					30			

gtt	tat	gga	gat	att	ggg	aca	agc	cca	ctc	tat	acg	atg	caa	tca	ttg	144
Val	Tyr	Gly	Asp	Ile	Gly	Thr	Ser	Pro	Leu	Tyr	Thr	Met	Gln	Ser	Leu	
		35				40					45					

gtt	gaa	aac	caa	ggg	ggg	att	tct	agt	gtc	aca	gaa	tcg	ttt	atc	tta	192
Val	Glu	Asn	Gln	Gly	Gly	Ile	Ser	Ser	Val	Thr	Glu	Ser	Phe	Ile	Leu	
	50					55					60					

ggg	tct	ata	tct	tta	atc	ata	tgg	acc	ttg	aca	ctt	att	aca	act	atc	240
Gly	Ser	Ile	Ser	Leu	Ile	Ile	Trp	Thr	Leu	Thr	Leu	Ile	Thr	Thr	Ile	
65					70				75						80	

aag	tat	gtg	ctt	gta	gct	tta	aag	gcg	gat	aat	cac	cac	gaa	ggg	ggg	288
Lys	Tyr	Val	Leu	Val	Ala	Leu	Lys	Ala	Asp	Asn	His	His	Glu	Gly	Gly	
				85				90						95		

att	ttt	tct	tta	tat	acc	ctt	gtt	aga	aaa	atg	aca	cct	tgg	tta	att	336
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Ile Phe Ser Leu Tyr Thr Leu Val Arg Lys Met Thr Pro Trp Leu Ile	
100 105 110	
gtt ccg gct gtt att gga ggt gca acc ttg ttg tca gat gga gct ttg	384
Val Pro Ala Val Ile Gly Gly Ala Thr Leu Leu Ser Asp Gly Ala Leu	
115 120 125	
acg cca gct gta acc gta ctt cag ccg tta agg att aaa gta gtt cct	432
Thr Pro Ala Val Thr Val Leu Gln Pro Leu Arg Ile Lys Val Val Pro	
130 135 140	
agt ttg cag cat att tcc aga atc aga gta tgt tat ttt gcg acc ttg	480
Ser Leu Gln His Ile Ser Arg Ile Arg Val Cys Tyr Phe Ala Thr Leu	
145 150 155 160	
tta ttt act gtt act ttt gcc atc caa ggt ttg gaa cgg gtg tta ttg	528
Leu Phe Thr Val Thr Phe Ala Ile Gln Gly Leu Glu Arg Val Leu Leu	
165 170 175	
gaa tta ttg gcc att atg tta tat ggt ttg cct ttt ggt tta	570
Glu Leu Leu Ala Ile Met Leu Tyr Gly Leu Pro Phe Gly Leu	
180 185 190	
ncggtctcct tatagttttg cccatccaga agttttcaag cattaatcca tactacggtt	630
tgaaattggtt atttagtcca gagaatcata aaggatatttt tatttttag gat cta ttt	687
Asp Leu Phe	
tcc tgg cga caa acg gga gca gaa gca cta tac tct gac tta ggt cat	735
Ser Trp Arg Gln Thr Gly Ala Glu Ala Leu Tyr Ser Asp Leu Gly His	
195 200 205	
gtt ggg cgt gga aat ata cat gtt tca tgg ccg ttc gtt aag gtt gcc	783
Val Gly Arg Gly Asn Ile His Val Ser Trp Pro Phe Val Lys Val Ala	
210 215 220 225	
att ata ctt tct tat tgt ggg caa ggg gca tgg att tta gct aat aag	831
Ile Ile Leu Ser Tyr Cys Gly Gln Gly Ala Trp Ile Leu Ala Asn Lys	
230 235 240	
aac gca gga aat gaa ttg aat ccc ttt ttt gct agt att cct tcg caa	879
Asn Ala Gly Asn Glu Leu Asn Pro Phe Phe Ala Ser Ile Pro Ser Gln	
245 250 255	
ttt aca atg cat gtc gtt att tta gct act ttg gca gct atc atc gct	927
Phe Thr Met His Val Val Ile Leu Ala Thr Leu Ala Ala Ile Ile Ala	
260 265 270	
tca cag gca ctg att tct ggatcaattt accttaagtt ctgagctatg	975

Ser Gln Ala Leu Ile Ser
275

cgactaaaaa tattcccaca atttcgttca acttatcctg ttgacaatat tgggtcaaac 1035
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taagacttca gcgcacatgg aagcagcata tggattagcg ataacaatta cgatgcta 1155
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tt 1217

<210> 10

<211> 190

<212> PRT

<213> Streptococcus agalactiae

<400> 10

Tyr Tyr Leu Ile Gly Gly Leu Ala Glu Met Gln His Val Asn His Ser
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Ser Phe Asp Lys Ala Ser Lys Ala Gly Phe Ile Ile Ala Leu Gly Ile
20 25 30

Val Tyr Gly Asp Ile Gly Thr Ser Pro Leu Tyr Thr Met Gln Ser Leu
35 40 45

Val Glu Asn Gln Gly Gly Ile Ser Ser Val Thr Glu Ser Phe Ile Leu
50 55 60

Gly Ser Ile Ser Leu Ile Ile Trp Thr Leu Thr Leu Ile Thr Thr Ile
65 70 75 80

Lys Tyr Val Leu Val Ala Leu Lys Ala Asp Asn His His Glu Gly Gly
85 90 95

Ile Phe Ser Leu Tyr Thr Leu Val Arg Lys Met Thr Pro Trp Leu Ile
 100 105 110

Val Pro Ala Val Ile Gly Gly Ala Thr Leu Leu Ser Asp Gly Ala Leu
 115 120 125

Thr Pro Ala Val Thr Val Leu Gln Pro Leu Arg Ile Lys Val Val Pro
 130 135 140

Ser Leu Gln His Ile Ser Arg Ile Arg Val Cys Tyr Phe Ala Thr Leu
 145 150 155 160

Leu Phe Thr Val Thr Phe Ala Ile Gln Gly Leu Glu Arg Val Leu Leu
 165 170 175

Glu Leu Leu Ala Ile Met Leu Tyr Gly Leu Pro Phe Gly Leu
 180 185 190

<210> 11

<211> 89

<212> PRT

<213> Streptococcus agalactiae

<400> 11

Asp Leu Phe Ser Trp Arg Gln Thr Gly Ala Glu Ala Leu Tyr Ser Asp
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Leu Gly His Val Gly Arg Gly Asn Ile His Val Ser Trp Pro Phe Val
 20 25 30

Lys Val Ala Ile Ile Leu Ser Tyr Cys Gly Gln Gly Ala Trp Ile Leu
 35 40 45

Ala Asn Lys Asn Ala Gly Asn Glu Leu Asn Pro Phe Phe Ala Ser Ile
 50 55 60

Pro Ser Gln Phe Thr Met His Val Val Ile Leu Ala Thr Leu Ala Ala
65 70 75 80

Ile Ile Ala Ser Gln Ala Leu Ile Ser
85

<210> 12

<211> 378

<212> DNA

<213> Streptococcus agalactiae

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<221> CDS

<222> (1) .. (378)

<223>

<400> 12

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Met Gln Val Phe Leu Asn Ile Val Asn Lys Phe Phe Asp Pro Val Ile
1 5 10 15

cat atg ggt tcg gga gtt gtg atg cta att gtc atg aca ggt tta gcc 96
His Met Gly Ser Gly Val Val Met Leu Ile Val Met Thr Gly Leu Ala
20 25 30

atg ata ttt gga gtg aag ttt tct aaa gca ctt gaa ggt ggt att aag 144
Met Ile Phe Gly Val Lys Phe Ser Lys Ala Leu Glu Gly Gly Ile Lys
35 40 45

tta gct att gct ctt acg ggt att ggt gct att att ggt att tta act 192
Leu Ala Ile Ala Leu Thr Gly Ile Gly Ala Ile Ile Gly Ile Leu Thr
50 55 60

ggt gct ttt tcc gaa tca ctt caa gct ttt gtt aaa aat aca gga atc 240
Gly Ala Phe Ser Glu Ser Leu Gln Ala Phe Val Lys Asn Thr Gly Ile
65 70 75 80

aat cta agc att att gac gtt ggt tgg gct cca tta gca act att aca 288

Asn Leu Ser Ile Ile Asp Val Gly Trp Ala Pro Leu Ala Thr Ile Thr
 85 90 95

tgg gga tca cca tat acg ctt tac ttc tta tta atc atg ctt att gtc 336
 Trp Gly Ser Pro Tyr Thr Leu Tyr Phe Leu Leu Ile Met Leu Ile Val
 100 105 110

aat att gtt atg att gtt atg aaa aaa aaa cgg ata cct tag 378
 Asn Ile Val Met Ile Val Met Lys Lys Lys Arg Ile Pro
 115 120 125

<210> 13

<211> 125

<212> PRT

<213> Streptococcus agalactiae

<400> 13

Met Gln Val Phe Leu Asn Ile Val Asn Lys Phe Phe Asp Pro Val Ile
 1 5 10 15

His Met Gly Ser Gly Val Val Met Leu Ile Val Met Thr Gly Leu Ala
 20 25 30

Met Ile Phe Gly Val Lys Phe Ser Lys Ala Leu Glu Gly Gly Ile Lys
 35 40 45

Leu Ala Ile Ala Leu Thr Gly Ile Gly Ala Ile Ile Gly Ile Leu Thr
 50 55 60

Gly Ala Phe Ser Glu Ser Leu Gln Ala Phe Val Lys Asn Thr Gly Ile
 65 70 75 80

Asn Leu Ser Ile Ile Asp Val Gly Trp Ala Pro Leu Ala Thr Ile Thr
 85 90 95

Trp Gly Ser Pro Tyr Thr Leu Tyr Phe Leu Leu Ile Met Leu Ile Val
 100 105 110

Asn Ile Val Met Ile Val Met Lys Lys Lys Arg Ile Pro
 115 120 125

<210> 14

<211> 705

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (118)..(705)

<223>

<400> 14

ggatcgggcg caagcttaac gattctttttt aaaatcatta aatttttaaaa caaatttcag 60

acatattgcc aaagttttga tattattact ataatatagt ttgtagagga gaataat 117

atg ggc caa gaa cct atc atc gaa tat caa aat atc aat aaa gtg tat 165
 Met Gly Gln Glu Pro Ile Ile Glu Tyr Gln Asn Ile Asn Lys Val Tyr
 1 5 10 15

ggg gaa aat gtt gcg gtt gaa gat att aac ctt aaa att tac cct ggt 213
 Gly Glu Asn Val Ala Val Glu Asp Ile Asn Leu Lys Ile Tyr Pro Gly
 20 25 30

gat ttc gtt tgt ttc atc ggt acg agt gga tca ggt aaa aca aca tta 261
 Asp Phe Val Cys Phe Ile Gly Thr Ser Gly Ser Gly Lys Thr Thr Leu
 35 40 45

atg cgt atg gtt aac cat atg tta aaa cca aca aat ggt act cta tta 309
 Met Arg Met Val Asn His Met Leu Lys Pro Thr Asn Gly Thr Leu Leu
 50 55 60

ttt aag gga aaa gat atc tct act att aac ccc att gaa tta aga cgc 357
 Phe Lys Gly Lys Asp Ile Ser Thr Ile Asn Pro Ile Glu Leu Arg Arg
 65 70 75 80

aga att gga tat gtt atc caa aac att ggt tta atg cct cat atg acc 405

Arg	Ile	Gly	Tyr	Val	Ile	Gln	Asn	Ile	Gly	Leu	Met	Pro	His	Met	Thr		
				85					90					95			
att	tac	gaa	aat	ata	gtt	ctt	gta	cca	aaa	tta	ttg	aaa	tgg	tca	gaa	453	
Ile	Tyr	Glu	Asn	Ile	Val	Leu	Val	Pro	Lys	Leu	Leu	Lys	Trp	Ser	Glu		
			100					105					110				
gaa	gct	aaa	aga	gct	aaa	gca	agg	gaa	ctt	att	aaa	tta	gtt	gaa	tta	501	
Glu	Ala	Lys	Arg	Ala	Lys	Ala	Arg	Glu	Leu	Ile	Lys	Leu	Val	Glu	Leu		
			115				120					125					
ccc	gaa	gaa	tat	ttg	gat	cgc	tac	cct	agt	gag	ttg	tct	ggc	ggg	cag	549	
Pro	Glu	Glu	Tyr	Leu	Asp	Arg	Tyr	Pro	Ser	Glu	Leu	Ser	Gly	Gly	Gln		
			130				135				140						
caa	caa	cgt	atc	ggg	gtc	att	cgc	gct	ctt	gca	gca	gac	caa	gat	att	597	
Gln	Gln	Arg	Ile	Gly	Val	Ile	Arg	Ala	Leu	Ala	Ala	Asp	Gln	Asp	Ile		
			145			150				155				160			
att	tta	atg	gat	gag	cct	ttt	gga	gct	ctg	gat	cct	att	act	aga	gaa	645	
Ile	Leu	Met	Asp	Glu	Pro	Phe	Gly	Ala	Leu	Asp	Pro	Ile	Thr	Arg	Glu		
			165					170					175				
ggg	att	caa	gac	ttt	agt	caa	gtc	tct	tca	gga	aga	aat	ggg	gga	aaa	693	
Gly	Ile	Gln	Asp	Phe	Ser	Gln	Val	Ser	Ser	Gly	Arg	Asn	Gly	Gly	Lys		
			180					185					190				
cta	tca	tct	tag													705	
Leu	Ser	Ser															
			195														

<210> 15

<211> 195

<212> PRT

<213> Streptococcus agalactiae

<400> 15

Met	Gly	Gln	Glu	Pro	Ile	Ile	Glu	Tyr	Gln	Asn	Ile	Asn	Lys	Val	Tyr
1				5					10					15	
Gly	Glu	Asn	Val	Ala	Val	Glu	Asp	Ile	Asn	Leu	Lys	Ile	Tyr	Pro	Gly
			20					25					30		

Asp Phe Val Cys Phe Ile Gly Thr Ser Gly Ser Gly Lys Thr Thr Leu
 35 40 45

Met Arg Met Val Asn His Met Leu Lys Pro Thr Asn Gly Thr Leu Leu
 50 55 60

Phe Lys Gly Lys Asp Ile Ser Thr Ile Asn Pro Ile Glu Leu Arg Arg
 65 70 75 80

Arg Ile Gly Tyr Val Ile Gln Asn Ile Gly Leu Met Pro His Met Thr
 85 90 95

Ile Tyr Glu Asn Ile Val Leu Val Pro Lys Leu Leu Lys Trp Ser Glu
 100 105 110

Glu Ala Lys Arg Ala Lys Ala Arg Glu Leu Ile Lys Leu Val Glu Leu
 115 120 125

Pro Glu Glu Tyr Leu Asp Arg Tyr Pro Ser Glu Leu Ser Gly Gly Gln
 130 135 140

Gln Gln Arg Ile Gly Val Ile Arg Ala Leu Ala Ala Asp Gln Asp Ile
 145 150 155 160

Ile Leu Met Asp Glu Pro Phe Gly Ala Leu Asp Pro Ile Thr Arg Glu
 165 170 175

Gly Ile Gln Asp Phe Ser Gln Val Ser Ser Gly Arg Asn Gly Gly Lys
 180 185 190

Leu Ser Ser
 195

<210> 16

<211> 367

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (366)

<223>

<400> 16

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Ile	Pro	Tyr	Ser	Asp	Val	Phe	Ala	Thr	Gly	Gly	Phe	Leu	Tyr	Tyr	Val	
1			5						10				15			

acg	att	gct	cta	agt	tac	ctt	tta	ggg	tct	agt	atc	tgg	tta	ttt	att	96
Thr	Ile	Ala	Leu	Ser	Tyr	Leu	Leu	Gly	Ser	Ser	Ile	Trp	Leu	Phe	Ile	
		20						25					30			

gta	cag	ttt	att	gct	tac	tat	gta	tct	gga	att	tat	ttt	tat	aaa	tta	144
Val	Gln	Phe	Ile	Ala	Tyr	Tyr	Val	Ser	Gly	Ile	Tyr	Phe	Tyr	Lys	Leu	
	35						40					45				

gtt	tat	tat	gtg	gca	caa	agt	gaa	att	gtc	tcg	ata	ggc	atg	acg	ttg	192
Val	Tyr	Tyr	Val	Ala	Gln	Ser	Glu	Ile	Val	Ser	Ile	Gly	Met	Thr	Leu	
	50					55					60					

att	ttc	tat	ata	atg	aat	att	gtc	tta	gga	ttc	ggg	ggg	atg	tac	cca	240
Ile	Phe	Tyr	Ile	Met	Asn	Ile	Val	Leu	Gly	Phe	Gly	Gly	Met	Tyr	Pro	
65				70					75					80		

ata	cag	tgg	gca	tta	cct	ttt	atg	ctc	att	tcg	cta	tgg	ttt	tta	att	288
Ile	Gln	Trp	Ala	Leu	Pro	Phe	Met	Leu	Ile	Ser	Leu	Trp	Phe	Leu	Ile	
			85						90				95			

aaa	ttt	tgt	gtc	gat	aat	atc	gtt	gat	gaa	gca	ttt	ata	ttt	tat	ggg	336
Lys	Phe	Cys	Val	Asp	Asn	Ile	Val	Asp	Glu	Ala	Phe	Ile	Phe	Tyr	Gly	
			100					105					110			

att	tta	gca	gca	ttc	tca	cta	ttt	ata	gat	c						367
Ile	Leu	Ala	Ala	Phe	Ser	Leu	Phe	Ile	Asp							
		115					120									

<210> 17

<211> 122

<212> PRT

<213> Streptococcus agalactiae

<400> 17

Ile Pro Tyr Ser Asp Val Phe Ala Thr Gly Gly Phe Leu Tyr Tyr Val
1 5 10 15

Thr Ile Ala Leu Ser Tyr Leu Leu Gly Ser Ser Ile Trp Leu Phe Ile
20 25 30

Val Gln Phe Ile Ala Tyr Tyr Val Ser Gly Ile Tyr Phe Tyr Lys Leu
35 40 45

Val Tyr Tyr Val Ala Gln Ser Glu Ile Val Ser Ile Gly Met Thr Leu
50 55 60

Ile Phe Tyr Ile Met Asn Ile Val Leu Gly Phe Gly Gly Met Tyr Pro
65 70 75 80

Ile Gln Trp Ala Leu Pro Phe Met Leu Ile Ser Leu Trp Phe Leu Ile
85 90 95

Lys Phe Cys Val Asp Asn Ile Val Asp Glu Ala Phe Ile Phe Tyr Gly
100 105 110

Ile Leu Ala Ala Phe Ser Leu Phe Ile Asp
115 120

<210> 18

<211> 570

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<223>

caa gat agt ggt ttt gat aat gac aaa aag tac gct aaa aaa atg acg 528
Gln Asp Ser Gly Phe Asp Asn Asp Lys Lys Tyr Ala Lys Lys Met Thr
165 170 175

gaa atc att gat ttg tat gat tta aca aga tat gat aag tga
 Glu Ile Ile Asp Leu Tyr Asp Leu Thr Arg Tyr Asp Lys
 180 185

570

<210> 19

<211> 189

<212> PRT

<213> Streptococcus agalactiae

<400> 19

Met Arg Lys Arg Phe Ser Leu Leu Asn Phe Ile Val Val Thr Phe Ile
 1 5 10 15

Phe Phe Phe Phe Ile Leu Phe Pro Leu Leu Asn His Lys Gly Lys Val
 20 25 30

Asp Ala Asn Ser Arg Gln Ser Val Thr Tyr Thr Lys Glu Glu Phe Ile
 35 40 45

Gln Lys Ile Val Pro Asp Ala Gln Asp Leu Gly Lys Ser Tyr Gly Ile
 50 55 60

Arg Pro Ser Phe Ile Ile Ala Gln Ala Ala Leu Asp Ser Asp Phe Gly
 65 70 75 80

Glu Lys Tyr Ser Tyr Ser Ile Ile Ile Cys Trp Leu Leu Ala Glu Pro
 85 90 95

Gly Thr Pro Ser Ile Thr Leu Asn Asp Ser Ser Thr Gly Lys Lys Gln
 100 105 110

Glu Lys Gln Phe Thr His Tyr Lys Ser Trp Lys Tyr Ser Met Asp Asp
 115 120 125

Tyr Leu Ala His Ile Lys Ser Gly Ala Thr Gly Lys Lys Asp Ser Tyr
 130 135 140

Thr Ile Met Val Ser Val Lys Asn Pro Lys Thr Leu Val Gln Lys Leu
 145 150 155 160

Gln Asp Ser Gly Phe Asp Asn Asp Lys Lys Tyr Ala Lys Lys Met Thr
 165 170 175

Glu Ile Ile Asp Leu Tyr Asp Leu Thr Arg Tyr Asp Lys
 180 185

<210> 20

<211> 978

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (978)

<223>

<400> 20

atg ctt gtc atc att ttg atc att gta cta gct agt ctg aca gtg acg 48
 Met Leu Val Ile Ile Leu Ile Ile Val Leu Ala Ser Leu Thr Val Thr
 1 5 10 15

ata att tct tac cca aaa atg acg gaa tta aca aag tcc gtt gaa aaa 96
 Ile Ile Ser Tyr Pro Lys Met Thr Glu Leu Thr Lys Ser Val Glu Lys
 20 25 30

caa ctt gaa gat aat gct gat aat cta tca gac caa ctg aca tat cag 144
 Gln Leu Glu Asp Asn Ala Asp Asn Leu Ser Asp Gln Leu Thr Tyr Gln
 35 40 45

ata gaa gtg gcg caa aaa gat caa atc tac gtg act aat cag cta aac 192
 Ile Glu Val Ala Gln Lys Asp Gln Ile Tyr Val Thr Asn Gln Leu Asn
 50 55 60

cgt atg caa cag gaa att atc agt cgc tta ccg ata tgc gta cag aat 240

Arg Met Gln Gln Glu Ile Ile Ser Arg Leu Pro Ile Cys Val Gln Asn	
65 70 75 80	
aaa tca gca tta acg gag agt cga gat cga tca gac aaa cgc ttg gaa	288
Lys Ser Ala Leu Thr Glu Ser Arg Asp Arg Ser Asp Lys Arg Leu Glu	
85 90 95	
ttg att aac tcc aat tta tct cag tca gtt cag aaa atg caa gat tca	336
Leu Ile Asn Ser Asn Leu Ser Gln Ser Val Gln Lys Met Gln Asp Ser	
100 105 110	
atg aaa aac gct tgg atc aaa tgc gcc aaa ctg ttg agg aaa agc tgg	384
Met Lys Asn Ala Trp Ile Lys Cys Ala Lys Leu Leu Arg Lys Ser Trp	
115 120 125	
aaa aaa cgc tac aaa cgc gtt gca aac ttc ttt gaa act gta tcg cgt	432
Lys Lys Arg Tyr Lys Arg Val Ala Asn Phe Phe Glu Thr Val Ser Arg	
130 135 140	
caa cta gag agc gtc aat caa ggt ctg ggt aga tgg aaa ctg tgc caa	480
Gln Leu Glu Ser Val Asn Gln Gly Leu Gly Arg Trp Lys Leu Cys Gln	
145 150 155 160	
gat gtt ggt acc act gaa caa agt ctg tca aat act aag aca agg gga	528
Asp Val Gly Thr Thr Glu Gln Ser Leu Ser Asn Thr Lys Thr Arg Gly	
165 170 175	
ata tta ggg gag tta caa ctc ggt caa att ata gaa gat att atg aca	576
Ile Leu Gly Glu Leu Gln Leu Gly Gln Ile Ile Glu Asp Ile Met Thr	
180 185 190	
gtt agt caa tat gag aga gaa ttt cct acg gtg tct ggc tct tct gag	624
Val Ser Gln Tyr Glu Arg Glu Phe Pro Thr Val Ser Gly Ser Ser Glu	
195 200 205	
cgt gtt gaa tat gct att aaa tac ctg gaa atg gtc agg gag att ata	672
Arg Val Glu Tyr Ala Ile Lys Tyr Leu Glu Met Val Arg Glu Ile Ile	
210 215 220	
tct att tgc cta ttg act cta agt ttc tct aga aga tta tta ccg att	720
Ser Ile Cys Leu Leu Thr Leu Ser Phe Ser Arg Arg Leu Leu Pro Ile	
225 230 235 240	
ggg aga tgc tta tgg aat tgg gtg acc agg ttc aaa tgg aac tct att	768
Gly Arg Cys Leu Trp Asn Trp Val Thr Arg Phe Lys Trp Asn Ser Ile	
245 250 255	
cgt aat ctt tac tgg gca agt att cgt aaa ttt gca aaa gat ata aac	816
Arg Asn Leu Tyr Trp Ala Ser Ile Arg Lys Phe Ala Lys Asp Ile Asn	
260 265 270	

aat aag tac tta aat cct cct gaa acg aca aat ttt ggt atc atg ttc 864
 Asn Lys Tyr Leu Asn Pro Pro Glu Thr Thr Asn Phe Gly Ile Met Phe
 275 280 285

tta cca act gaa ggg ctc tat tct gaa gtg gta aga aat gca aca ttc 912
 Leu Pro Thr Glu Gly Leu Tyr Ser Glu Val Val Arg Asn Ala Thr Phe
 290 295 300

ttt gat agt cta aga cgt gac gaa aat att gta gta gct gga ccg tca 960
 Phe Asp Ser Leu Arg Arg Asp Glu Asn Ile Val Val Ala Gly Pro Ser
 305 310 315 320

acc tta tct gct tac taa 978
 Thr Leu Ser Ala Tyr
 325

<210> 21

<211> 325

<212> PRT

<213> Streptococcus agalactiae

<400> 21

Met Leu Val Ile Ile Leu Ile Ile Val Leu Ala Ser Leu Thr Val Thr
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Ile Ile Ser Tyr Pro Lys Met Thr Glu Leu Thr Lys Ser Val Glu Lys
 20 25 30

Gln Leu Glu Asp Asn Ala Asp Asn Leu Ser Asp Gln Leu Thr Tyr Gln
 35 40 45

Ile Glu Val Ala Gln Lys Asp Gln Ile Tyr Val Thr Asn Gln Leu Asn
 50 55 60

Arg Met Gln Gln Glu Ile Ile Ser Arg Leu Pro Ile Cys Val Gln Asn
 65 70 75 80

Lys Ser Ala Leu Thr Glu Ser Arg Asp Arg Ser Asp Lys Arg Leu Glu
 85 90 95

Leu Ile Asn Ser Asn Leu Ser Gln Ser Val Gln Lys Met Gln Asp Ser
 100 105 110

Met Lys Asn Ala Trp Ile Lys Cys Ala Lys Leu Leu Arg Lys Ser Trp
 115 120 125

Lys Lys Arg Tyr Lys Arg Val Ala Asn Phe Phe Glu Thr Val Ser Arg
 130 135 140

Gln Leu Glu Ser Val Asn Gln Gly Leu Gly Arg Trp Lys Leu Cys Gln
 145 150 155 160

Asp Val Gly Thr Thr Glu Gln Ser Leu Ser Asn Thr Lys Thr Arg Gly
 165 170 175

Ile Leu Gly Glu Leu Gln Leu Gly Gln Ile Ile Glu Asp Ile Met Thr
 180 185 190

Val Ser Gln Tyr Glu Arg Glu Phe Pro Thr Val Ser Gly Ser Ser Glu
 195 200 205

Arg Val Glu Tyr Ala Ile Lys Tyr Leu Glu Met Val Arg Glu Ile Ile
 210 215 220

Ser Ile Cys Leu Leu Thr Leu Ser Phe Ser Arg Arg Leu Leu Pro Ile
 225 230 235 240

Gly Arg Cys Leu Trp Asn Trp Val Thr Arg Phe Lys Trp Asn Ser Ile
 245 250 255

Arg Asn Leu Tyr Trp Ala Ser Ile Arg Lys Phe Ala Lys Asp Ile Asn
 260 265 270

Asn Lys Tyr Leu Asn Pro Pro Glu Thr Thr Asn Phe Gly Ile Met Phe
 275 280 285

Leu Pro Thr Glu Gly Leu Tyr Ser Glu Val Val Arg Asn Ala Thr Phe
 290 295 300

Phe Asp Ser Leu Arg Arg Asp Glu Asn Ile Val Val Ala Gly Pro Ser
 305 310 315 320

Thr Leu Ser Ala Tyr
 325

<210> 22

<211> 579

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (579)

<223>

<400> 22

atg cga aaa gaa gtg aca cca gag atg ctt aac tat aat aag tat cct 48
 Met Arg Lys Glu Val Thr Pro Glu Met Leu Asn Tyr Asn Lys Tyr Pro
 1 5 10 15

ggc cca cag ttt att cac ttt gaa aat atc gtt aaa agt gat gat att 96
 Gly Pro Gln Phe Ile His Phe Glu Asn Ile Val Lys Ser Asp Asp Ile
 20 25 30

gaa ttt caa ctt gtt att aat gaa aaa tca gct ttt gat gtg act gtc 144
 Glu Phe Gln Leu Val Ile Asn Glu Lys Ser Ala Phe Asp Val Thr Val
 35 40 45

ttt gga caa cgt ttt tct gag att tta tta aaa tat gat ttt atc gtt 192
 Phe Gly Gln Arg Phe Ser Glu Ile Leu Leu Lys Tyr Asp Phe Ile Val
 50 55 60

ggc gat tgg ggt aac gag cag ttg agg cta aga ggc ttt tac aaa gat 240
 Gly Asp Trp Gly Asn Glu Gln Leu Arg Leu Arg Gly Phe Tyr Lys Asp
 65 70 75 80

gct agt acg att aga aaa aat agc cgg att tca cgt tta gaa gat tat 288

Ala	Ser	Thr	Ile	Arg	Lys	Asn	Ser	Arg	Ile	Ser	Arg	Leu	Glu	Asp	Tyr		
				85					90					95			
att	aaa	gag	tat	tgt	aac	ttt	ggg	tgt	gct	tat	ttt	gtg	ttg	gag	aat	336	
Ile	Lys	Glu	Tyr	Cys	Asn	Phe	Gly	Cys	Ala	Tyr	Phe	Val	Leu	Glu	Asn		
			100					105					110				
cca	aat	cct	aga	gat	att	aaa	ttt	gat	gat	gaa	aga	cct	cat	aag	cgt	384	
Pro	Asn	Pro	Arg	Asp	Ile	Lys	Phe	Asp	Asp	Glu	Arg	Pro	His	Lys	Arg		
			115					120					125				
cgt	aag	tca	aga	tcc	aaa	tca	caa	tca	tca	aag	tca	caa	act	aga	aat	432	
Arg	Lys	Ser	Arg	Ser	Lys	Ser	Gln	Ser	Ser	Lys	Ser	Gln	Thr	Arg	Asn		
			130					135					140				
aat	cgt	tcc	cag	tca	aat	gcc	aat	gct	cat	ttt	aca	agt	aaa	aag	cgt	480	
Asn	Arg	Ser	Gln	Ser	Asn	Ala	Asn	Ala	His	Phe	Thr	Ser	Lys	Lys	Arg		
					150					155					160		
aaa	gac	aca	aaa	cgc	cgt	caa	gaa	cgt	cat	att	aaa	gaa	gag	caa	gat	528	
Lys	Asp	Thr	Lys	Arg	Arg	Gln	Glu	Arg	His	Ile	Lys	Glu	Glu	Gln	Asp		
				165					170					175			
aag	gaa	atg	acc	tct	gca	aag	cag	cat	ttg	tta	ttc	gta	aga	aaa	aat	576	
Lys	Glu	Met	Thr	Ser	Ala	Lys	Gln	His	Leu	Leu	Phe	Val	Arg	Lys	Asn		
				180				185					190				
taa																579	

<210> 23

<211> 192

<212> PRT

<213> Streptococcus agalactiae

<400> 23

Met	Arg	Lys	Glu	Val	Thr	Pro	Glu	Met	Leu	Asn	Tyr	Asn	Lys	Tyr	Pro
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Gly	Pro	Gln	Phe	Ile	His	Phe	Glu	Asn	Ile	Val	Lys	Ser	Asp	Asp	Ile
			20					25					30		

Glu Phe Gln Leu Val Ile Asn Glu Lys Ser Ala Phe Asp Val Thr Val
 35 40 45

Phe Gly Gln Arg Phe Ser Glu Ile Leu Leu Lys Tyr Asp Phe Ile Val
 50 55 60

Gly Asp Trp Gly Asn Glu Gln Leu Arg Leu Arg Gly Phe Tyr Lys Asp
 65 70 75 80

Ala Ser Thr Ile Arg Lys Asn Ser Arg Ile Ser Arg Leu Glu Asp Tyr
 85 90 95

Ile Lys Glu Tyr Cys Asn Phe Gly Cys Ala Tyr Phe Val Leu Glu Asn
 100 105 110

Pro Asn Pro Arg Asp Ile Lys Phe Asp Asp Glu Arg Pro His Lys Arg
 115 120 125

Arg Lys Ser Arg Ser Lys Ser Gln Ser Ser Lys Ser Gln Thr Arg Asn
 130 135 140

Asn Arg Ser Gln Ser Asn Ala Asn Ala His Phe Thr Ser Lys Lys Arg
 145 150 155 160

Lys Asp Thr Lys Arg Arg Gln Glu Arg His Ile Lys Glu Glu Gln Asp
 165 170 175

Lys Glu Met Thr Ser Ala Lys Gln His Leu Leu Phe Val Arg Lys Asn
 180 185 190

<210> 24

<211> 609

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (609)

<223>

<400> 24

atg aca ata aaa aaa gtg tta agt gta aca gga att att tta gtg aca	48
Met Thr Ile Lys Lys Val Leu Ser Val Thr Gly Ile Ile Leu Val Thr	
1 5 10 15	
gta gcg tct cta gct gct tgt agc tca aaa tct cat act act aag acg	96
Val Ala Ser Leu Ala Ala Cys Ser Ser Lys Ser His Thr Thr Lys Thr	
20 25 30	
ggc aaa aaa gaa gtt aat ttt gca act gtt gga aca acg gca cct ttt	144
Gly Lys Lys Glu Val Asn Phe Ala Thr Val Gly Thr Thr Ala Pro Phe	
35 40 45	
tct tat gtg aag gat ggg aaa ctg act ggc ttt gat att gaa gta gcc	192
Ser Tyr Val Lys Asp Gly Lys Leu Thr Gly Phe Asp Ile Glu Val Ala	
50 55 60	
aaa gct gtt ttt aaa ggt tca gat aac tat aaa gtc act ttt aaa aaa	240
Lys Ala Val Phe Lys Gly Ser Asp Asn Tyr Lys Val Thr Phe Lys Lys	
65 70 75 80	
aca gaa tgg tca tcg gta ttt acc ggc att gat tca gga aag ttt caa	288
Thr Glu Trp Ser Ser Val Phe Thr Gly Ile Asp Ser Gly Lys Phe Gln	
85 90 95	
atg ggt gga aat aat att tct tat tca tca gag aga tct caa aaa tay	336
Met Gly Gly Asn Asn Ile Ser Tyr Ser Ser Glu Arg Ser Gln Lys Tyr	
100 105 110	
tta ttt tca tac cca ata ggc tct act cct tca gtt tta gca gtt cct	384
Leu Phe Ser Tyr Pro Ile Gly Ser Thr Pro Ser Val Leu Ala Val Pro	
115 120 125	
aag aat agt aat atc aaa gct tat aat gat att agt ggt cat aaa aca	432
Lys Asn Ser Asn Ile Lys Ala Tyr Asn Asp Ile Ser Gly His Lys Thr	
130 135 140	
cag gtt gtc caa gga acg aca act gcc aag caa tta gaa aat ttc aat	480
Gln Val Val Gln Gly Thr Thr Thr Ala Lys Gln Leu Glu Asn Phe Asn	
145 150 155 160	
aaa gag cat cag aaa aat cct gtt act cta aaa tat act aat gaa aat	528

Lys Glu His Gln Lys Asn Pro Val Thr Leu Lys Tyr Thr Asn Glu Asn
 165 170 175

att aca cag att cta acg aat ttg agt gat gga aaa gct gat ttt aaa 576
 Ile Thr Gln Ile Leu Thr Asn Leu Ser Asp Gly Lys Ala Asp Phe Lys
 180 185 190

ctt ttg acg gac caa ctg tta acg cta tta taa 609
 Leu Leu Thr Asp Gln Leu Leu Thr Leu Leu
 195 200

<210> 25

<211> 202

<212> PRT

<213> Streptococcus agalactiae

<400> 25

Met Thr Ile Lys Lys Val Leu Ser Val Thr Gly Ile Ile Leu Val Thr
 1 5 10 15

Val Ala Ser Leu Ala Ala Cys Ser Ser Lys Ser His Thr Thr Lys Thr
 20 25 30

Gly Lys Lys Glu Val Asn Phe Ala Thr Val Gly Thr Thr Ala Pro Phe
 35 40 45

Ser Tyr Val Lys Asp Gly Lys Leu Thr Gly Phe Asp Ile Glu Val Ala
 50 55 60

Lys Ala Val Phe Lys Gly Ser Asp Asn Tyr Lys Val Thr Phe Lys Lys
 65 70 75 80

Thr Glu Trp Ser Ser Val Phe Thr Gly Ile Asp Ser Gly Lys Phe Gln
 85 90 95

Met Gly Gly Asn Asn Ile Ser Tyr Ser Ser Glu Arg Ser Gln Lys Tyr
 100 105 110

Leu Phe Ser Tyr Pro Ile Gly Ser Thr Pro Ser Val Leu Ala Val Pro
 115 120 125

Lys Asn Ser Asn Ile Lys Ala Tyr Asn Asp Ile Ser Gly His Lys Thr
 130 135 140

Gln Val Val Gln Gly Thr Thr Thr Ala Lys Gln Leu Glu Asn Phe Asn
 145 150 155 160

Lys Glu His Gln Lys Asn Pro Val Thr Leu Lys Tyr Thr Asn Glu Asn
 165 170 175

Ile Thr Gln Ile Leu Thr Asn Leu Ser Asp Gly Lys Ala Asp Phe Lys
 180 185 190

Leu Leu Thr Asp Gln Leu Leu Thr Leu Leu
 195 200

<210> 26

<211> 357

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (357)

<223>

<400> 26

atg aag aat ata aca aag cta tca act gtt gct tta agc cta cta ctt 48
 Met Lys Asn Ile Thr Lys Leu Ser Thr Val Ala Leu Ser Leu Leu Leu
 1 5 10 15

tgt acg gcg tgt gct gca tca aac acg tct aca tct aaa aca cag tct 96

Cys	Thr	Ala	Cys	Ala	Ala	Ser	Asn	Thr	Ser	Thr	Ser	Lys	Thr	Gln	Ser	
			20					25					30			
cat	cat	cct	aaa	caa	act	aaa	ctc	aca	gat	aag	caa	aaa	gaa	gaa	ccc	144
His	His	Pro	Lys	Gln	Thr	Lys	Leu	Thr	Asp	Lys	Gln	Lys	Glu	Glu	Pro	
		35					40				45					
aaa	aac	aaa	gaa	gct	gct	gat	caa	gag	atg	cat	ccc	caa	ggc	gct	gtt	192
Lys	Asn	Lys	Glu	Ala	Ala	Asp	Gln	Glu	Met	His	Pro	Gln	Gly	Ala	Val	
	50					55				60						
gat	ttg	aca	aaa	tat	aag	gca	aaa	ccg	gtc	aaa	gat	tat	gga	aaa	aaa	240
Asp	Leu	Thr	Lys	Tyr	Lys	Ala	Lys	Pro	Val	Lys	Asp	Tyr	Gly	Lys	Lys	
65					70				75					80		
atc	gat	gtt	ggg	gat	ggc	aag	aaa	atg	aac	att	tat	gaa	act	ggg	cag	288
Ile	Asp	Val	Gly	Asp	Gly	Lys	Lys	Met	Asn	Ile	Tyr	Glu	Thr	Gly	Gln	
				85				90						95		
gga	aaa	att	cca	att	gtt	ttt	att	cct	ggg	caa	gct	gag	att	cgc	cac	336
Gly	Lys	Ile	Pro	Ile	Val	Phe	Ile	Pro	Gly	Gln	Ala	Glu	Ile	Arg	His	
			100					105					110			
gct	atg	ctt	ata	aga	att	taa										357
Ala	Met	Leu	Ile	Arg	Ile											
			115													

<210> 27

<211> 118

<212> PRT

<213> Streptococcus agalactiae

<400> 27

Met	Lys	Asn	Ile	Thr	Lys	Leu	Ser	Thr	Val	Ala	Leu	Ser	Leu	Leu	Leu	
1				5					10				15			
Cys	Thr	Ala	Cys	Ala	Ala	Ser	Asn	Thr	Ser	Thr	Ser	Lys	Thr	Gln	Ser	
			20					25					30			
His	His	Pro	Lys	Gln	Thr	Lys	Leu	Thr	Asp	Lys	Gln	Lys	Glu	Glu	Pro	
		35					40				45					

Lys Asn Lys Glu Ala Ala Asp Gln Glu Met His Pro Gln Gly Ala Val
 50 55 60

Asp Leu Thr Lys Tyr Lys Ala Lys Pro Val Lys Asp Tyr Gly Lys Lys
 65 70 75 80

Ile Asp Val Gly Asp Gly Lys Lys Met Asn Ile Tyr Glu Thr Gly Gln
 85 90 95

Gly Lys Ile Pro Ile Val Phe Ile Pro Gly Gln Ala Glu Ile Arg His
 100 105 110

Ala Met Leu Ile Arg Ile
 115

<210> 28

<211> 1191

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (1191)

<223>

<400> 28

gtg aat gaa tcg acc atc aga aaa gaa ttt aaa ata gtt gtt ttt aaa 48
 Val Asn Glu Ser Thr Ile Arg Lys Glu Phe Lys Ile Val Val Phe Lys
 1 5 10 15

tgg atc tta aat aat caa gca gtt att gct ctc atg att acc ttt ttg 96
 Trp Ile Leu Asn Asn Gln Ala Val Ile Ala Leu Met Ile Thr Phe Leu
 20 25 30

gta ttt tta acg att ttt att ttt acc aaa atc tct ttt atg ttt aaa 144

Val Phe Leu Thr Ile Phe Ile Phe Thr Lys Ile Ser Phe Met Phe Lys	
35 40 45	
cct gtg ttt gat ttt ctt gct gtg ctg ata ttg ccg ctt gta att tct	192
Pro Val Phe Asp Phe Leu Ala Val Leu Ile Leu Pro Leu Val Ile Ser	
50 55 60	
ggc ttg ctt tat tac cta tta aaa cct atg gtt aca ttt tta gag aag	240
Gly Leu Leu Tyr Tyr Leu Leu Lys Pro Met Val Thr Phe Leu Glu Lys	
65 70 75 80	
cgg gga att aag cgt gta aca gcg ata tta tca gtt ttt act att ata	288
Arg Gly Ile Lys Arg Val Thr Ala Ile Leu Ser Val Phe Thr Ile Ile	
85 90 95	
atc ctt ctg tta att tgg gca atg tct agt ttt att ccc atg atg agt	336
Ile Leu Leu Leu Ile Trp Ala Met Ser Ser Phe Ile Pro Met Met Ser	
100 105 110	
aat caa tta cgc cat ttt atg gaa gat ctc cct tca tat gtg aat aaa	384
Asn Gln Leu Arg His Phe Met Glu Asp Leu Pro Ser Tyr Val Asn Lys	
115 120 125	
gtg caa atg gaa aca agt tcg ttt ata gat cac aac cct tgg tta aaa	432
Val Gln Met Glu Thr Ser Ser Phe Ile Asp His Asn Pro Trp Leu Lys	
130 135 140	
tct tat aaa ggg gaa ata tcg agc atg tta tct aat atc agt agc caa	480
Ser Tyr Lys Gly Glu Ile Ser Ser Met Leu Ser Asn Ile Ser Ser Gln	
145 150 155 160	
gcg gtc tct tat gct gaa aaa ttt tca aag aat gtt tta gat tgg gca	528
Ala Val Ser Tyr Ala Glu Lys Phe Ser Lys Asn Val Leu Asp Trp Ala	
165 170 175	
gga aat tta gct agt aca gtt gca cgt gtg aca gta gca aca atc atg	576
Gly Asn Leu Ala Ser Thr Val Ala Arg Val Thr Val Ala Thr Ile Met	
180 185 190	
gct ccc ttt att ttg ttt tat ctt tta aga gat agt cgc aac atg aag	624
Ala Pro Phe Ile Leu Phe Tyr Leu Leu Arg Asp Ser Arg Asn Met Lys	
195 200 205	
aat ggt ttc tta atg gtt tta cca acc aaa cta cgc caa cca gct gat	672
Asn Gly Phe Leu Met Val Leu Pro Thr Lys Leu Arg Gln Pro Ala Asp	
210 215 220	
cgt att ttg cga gaa atg aat agt caa atg tca gga tat gtg caa gga	720
Arg Ile Leu Arg Glu Met Asn Ser Gln Met Ser Gly Tyr Val Gln Gly	
225 230 235 240	

caa atc att gtt gct att act gtt ggt gtt att ttt tca ata atg tat	768
Gln Ile Ile Val Ala Ile Thr Val Gly Val Ile Phe Ser Ile Met Tyr	
245 250 255	
agt att ata ggc ctt aga tat ggc gtg aca tta ggg att att gcc ggt	816
Ser Ile Ile Gly Leu Arg Tyr Gly Val Thr Leu Gly Ile Ile Ala Gly	
260 265 270	
gtg tta aat atg gtt ccc tat ttg gga agt ttt gtc gcc caa att cca	864
Val Leu Asn Met Val Pro Tyr Leu Gly Ser Phe Val Ala Gln Ile Pro	
275 280 285	
gtg ttt atc tta gcg ctt gtc gca gga cct gtt atg gtt gtt aaa gtt	912
Val Phe Ile Leu Ala Leu Val Ala Gly Pro Val Met Val Val Lys Val	
290 295 300	
gcg att gtt ttt gtt att gag caa act cta gag gga cgc ttt gtc tca	960
Ala Ile Val Phe Val Ile Glu Gln Thr Leu Glu Gly Arg Phe Val Ser	
305 310 315 320	
cct ttg gtt tta ggt aat aaa ctt agc att cat cca att aca att atg	1008
Pro Leu Val Leu Gly Asn Lys Leu Ser Ile His Pro Ile Thr Ile Met	
325 330 335	
ttt att tta tta acc tct gga gcg atg ttt ggt gtt tgg gga gta ttc	1056
Phe Ile Leu Leu Thr Ser Gly Ala Met Phe Gly Val Trp Gly Val Phe	
340 345 350	
ctc agt att ccg att tat gca tct atc aaa gtt gtt gtt aaa gaa ttg	1104
Leu Ser Ile Pro Ile Tyr Ala Ser Ile Lys Val Val Val Lys Glu Leu	
355 360 365	
ttt gat tgg tac aaa gct gtc agt ggg cta tat aca ata gat gtt gtt	1152
Phe Asp Trp Tyr Lys Ala Val Ser Gly Leu Tyr Thr Ile Asp Val Val	
370 375 380	
act gaa gaa aga agt gaa gaa gtt aaa aat gtt gaa tag	1191
Thr Glu Glu Arg Ser Glu Glu Val Lys Asn Val Glu	
385 390 395	

<210> 29

<211> 396

<212> PRT

<213> Streptococcus agalactiae

<400> 29

Val Asn Glu Ser Thr Ile Arg Lys Glu Phe Lys Ile Val Val Phe Lys
 1 5 10 15

Trp Ile Leu Asn Asn Gln Ala Val Ile Ala Leu Met Ile Thr Phe Leu
 20 25 30

Val Phe Leu Thr Ile Phe Ile Phe Thr Lys Ile Ser Phe Met Phe Lys
 35 40 45

Pro Val Phe Asp Phe Leu Ala Val Leu Ile Leu Pro Leu Val Ile Ser
 50 55 60

Gly Leu Leu Tyr Tyr Leu Leu Lys Pro Met Val Thr Phe Leu Glu Lys
 65 70 75 80

Arg Gly Ile Lys Arg Val Thr Ala Ile Leu Ser Val Phe Thr Ile Ile
 85 90 95

Ile Leu Leu Leu Ile Trp Ala Met Ser Ser Phe Ile Pro Met Met Ser
 100 105 110

Asn Gln Leu Arg His Phe Met Glu Asp Leu Pro Ser Tyr Val Asn Lys
 115 120 125

Val Gln Met Glu Thr Ser Ser Phe Ile Asp His Asn Pro Trp Leu Lys
 130 135 140

Ser Tyr Lys Gly Glu Ile Ser Ser Met Leu Ser Asn Ile Ser Ser Gln
 145 150 155 160

Ala Val Ser Tyr Ala Glu Lys Phe Ser Lys Asn Val Leu Asp Trp Ala
 165 170 175

Gly Asn Leu Ala Ser Thr Val Ala Arg Val Thr Val Ala Thr Ile Met
 180 185 190

Ala Pro Phe Ile Leu Phe Tyr Leu Leu Arg Asp Ser Arg Asn Met Lys
 195 200 205

Asn Gly Phe Leu Met Val Leu Pro Thr Lys Leu Arg Gln Pro Ala Asp
 210 215 220

Arg Ile Leu Arg Glu Met Asn Ser Gln Met Ser Gly Tyr Val Gln Gly
 225 230 235 240

Gln Ile Ile Val Ala Ile Thr Val Gly Val Ile Phe Ser Ile Met Tyr
 245 250 255

Ser Ile Ile Gly Leu Arg Tyr Gly Val Thr Leu Gly Ile Ile Ala Gly
 260 265 270

Val Leu Asn Met Val Pro Tyr Leu Gly Ser Phe Val Ala Gln Ile Pro
 275 280 285

Val Phe Ile Leu Ala Leu Val Ala Gly Pro Val Met Val Val Lys Val
 290 295 300

Ala Ile Val Phe Val Ile Glu Gln Thr Leu Glu Gly Arg Phe Val Ser
 305 310 315 320

Pro Leu Val Leu Gly Asn Lys Leu Ser Ile His Pro Ile Thr Ile Met
 325 330 335

Phe Ile Leu Leu Thr Ser Gly Ala Met Phe Gly Val Trp Gly Val Phe
 340 345 350

Leu Ser Ile Pro Ile Tyr Ala Ser Ile Lys Val Val Val Lys Glu Leu
 355 360 365

Phe Asp Trp Tyr Lys Ala Val Ser Gly Leu Tyr Thr Ile Asp Val Val
 370 375 380

Thr Glu Glu Arg Ser Glu Glu Val Lys Asn Val Glu
 385 390 395

<210> 30

<211> 1230

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1)..(1230)

<223>

<220>

<221> misc_feature

<222> (357)..(357)

<223> The 'Xaa' at location 357 stands for Thr, or Ile.

<400> 30

atg	ttt	atg	gga	atc	cca	caa	tat	ttc	ttc	tac	ctt	atc	tta	gct	gtc	48
Met	Phe	Met	Gly	Ile	Pro	Gln	Tyr	Phe	Phe	Tyr	Leu	Ile	Leu	Ala	Val	
1			5					10					15			

cta	cca	att	tac	atc	ggc	tta	ttc	ttt	aag	aag	cgt	ttt	gcc	tta	tat	96
Leu	Pro	Ile	Tyr	Ile	Gly	Leu	Phe	Phe	Lys	Lys	Arg	Phe	Ala	Leu	Tyr	
			20				25						30			

gag	att	att	ttt	agt	cta	agt	ttt	att	gta	atg	atg	ttg	act	ggg	agt	144
Glu	Ile	Ile	Phe	Ser	Leu	Ser	Phe	Ile	Val	Met	Met	Leu	Thr	Gly	Ser	
			35				40					45				

act	ttt	aat	caa	ttg	aag	tca	cta	ttg	gca	tac	gtt	gtc	gga	cag	tct	192
Thr	Phe	Asn	Gln	Leu	Lys	Ser	Leu	Leu	Ala	Tyr	Val	Val	Gly	Gln	Ser	
			50				55				60					

ctg	cta	gtt	ttt	atc	tat	aaa	gct	tac	cgg	aaa	cga	ttt	aat	cat	act	240
Leu	Leu	Val	Phe	Ile	Tyr	Lys	Ala	Tyr	Arg	Lys	Arg	Phe	Asn	His	Thr	
65					70				75					80		

ttg	gtc	ttt	tat	gta	acg	gtt	tgt	tta	tct	att	ttt	ccg	cta	ttt	ttg	288
Leu	Val	Phe	Tyr	Val	Thr	Val	Cys	Leu	Ser	Ile	Phe	Pro	Leu	Phe	Leu	
				85				90						95		

gta aaa tta att cca gct ata tct gag gat ggg cat cag tca ctt ttt Val Lys Leu Ile Pro Ala Ile Ser Glu Asp Gly His Gln Ser Leu Phe 100 105 110	336
ggg ttt cta gga att tct tac ctt act ttt aga gct gtt gct atg att Gly Phe Leu Gly Ile Ser Tyr Leu Thr Phe Arg Ala Val Ala Met Ile 115 120 125	384
att gaa atg aga gac ggt gtc ttg aaa gaa ttt act tta tgg gaa ttc Ile Glu Met Arg Asp Gly Val Leu Lys Glu Phe Thr Leu Trp Glu Phe 130 135 140	432
tta aga ttt tta ctc ttc ttt cca act ttc tca agt gga cca att gat Leu Arg Phe Leu Leu Phe Phe Pro Thr Phe Ser Ser Gly Pro Ile Asp 145 150 155 160	480
cgt ttt aaa cga ttc aat gag gat tac att aat atc cca gat cga aac Arg Phe Lys Arg Phe Asn Glu Asp Tyr Ile Asn Ile Pro Asp Arg Asn 165 170 175	528
gaa ctc cta gat atg tta ggt caa gcg att cat tat ttg atg tta ggt Glu Leu Leu Asp Met Leu Gly Gln Ala Ile His Tyr Leu Met Leu Gly 180 185 190	576
ttt ctc tat aag ttt att tta gcc tat att ttt gga agt ctg att atg Phe Leu Tyr Lys Phe Ile Leu Ala Tyr Ile Phe Gly Ser Leu Ile Met 195 200 205	624
cct cct cta aaa gaa tta gcg cta gaa cag ggt ggt gtg ttt aat tgg Pro Pro Leu Lys Glu Leu Ala Leu Glu Gln Gly Gly Val Phe Asn Trp 210 215 220	672
cca aca ctt ggg gtt atg tat gcc ttt ggt ttt gat ttg ttc ttt gat Pro Thr Leu Gly Val Met Tyr Ala Phe Gly Phe Asp Leu Phe Phe Asp 225 230 235 240	720
ttt gca ggt tac aca atg ttt gcg ttg gct att tct aac cta atg ggg Phe Ala Gly Tyr Thr Met Phe Ala Leu Ala Ile Ser Asn Leu Met Gly 245 250 255	768
att aag tct ccg att aac ttt gac aaa cct ttc aaa tca cgc gac cta Ile Lys Ser Pro Ile Asn Phe Asp Lys Pro Phe Lys Ser Arg Asp Leu 260 265 270	816
aaa gaa ttt tgg aat aga tgg cat atg agc ctt tct ttc tgg ttt aga Lys Glu Phe Trp Asn Arg Trp His Met Ser Leu Ser Phe Trp Phe Arg 275 280 285	864
gac ttt gtt ttc atg agg ctt gtt aag ctt tta gtt aaa aat aaa gtt Asp Phe Val Phe Met Arg Leu Val Lys Leu Leu Val Lys Asn Lys Val 290 295 300	912

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ttt aaa aac cgt aat gtt act tca agt gta gct tat att atc aat atg      960
Phe Lys Asn Arg Asn Val Thr Ser Ser Val Ala Tyr Ile Ile Asn Met
305                      310                      315                      320

ctt ctt atg gga ttc tgg cat ggg tta act tgg tac tat ata gcc tat      1008
Leu Leu Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Ala Tyr
                      325                      330                      335

ggt ctc ttt cat ggg att ggc cta gtt att aat gac gct tgg gta cgt      1056
Gly Leu Phe His Gly Ile Gly Leu Val Ile Asn Asp Ala Trp Val Arg
                      340                      345                      350

aag aag aaa aat ayt aat aaa gaa aga aga ttg gct aaa aaa cca ctt      1104
Lys Lys Lys Asn Xaa Asn Lys Glu Arg Arg Leu Ala Lys Lys Pro Leu
                      355                      360                      365

tta cca gaa aac aaa tgg act tat gct ttg ggt gtc ttc atc acc ttt      1152
Leu Pro Glu Asn Lys Trp Thr Tyr Ala Leu Gly Val Phe Ile Thr Phe
                      370                      375                      380

aat gta gtt atg ttt tct ttc ttg att ttt tca gga ttt tta gat ctt      1200
Asn Val Val Met Phe Ser Phe Leu Ile Phe Ser Gly Phe Leu Asp Leu
385                      390                      395                      400

ttg tgg ttc cca caa ccg cat aac aaa taa      1230
Leu Trp Phe Pro Gln Pro His Asn Lys
                      405

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<210> 31

<211> 409

<212> PRT

<213> Streptococcus agalactiae

<220>

<221> misc_feature

<222> (357)..(357)

<223> The 'Xaa' at location 357 stands for Thr, or Ile.

<400> 31

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Met Phe Met Gly Ile Pro Gln Tyr Phe Phe Tyr Leu Ile Leu Ala Val
1                      5                      10                      15

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Leu Pro Ile Tyr Ile Gly Leu Phe Phe Lys Lys Arg Phe Ala Leu Tyr
 20 25 30

Glu Ile Ile Phe Ser Leu Ser Phe Ile Val Met Met Leu Thr Gly Ser
 35 40 45

Thr Phe Asn Gln Leu Lys Ser Leu Leu Ala Tyr Val Val Gly Gln Ser
 50 55 60

Leu Leu Val Phe Ile Tyr Lys Ala Tyr Arg Lys Arg Phe Asn His Thr
 65 70 75 80

Leu Val Phe Tyr Val Thr Val Cys Leu Ser Ile Phe Pro Leu Phe Leu
 85 90 95

Val Lys Leu Ile Pro Ala Ile Ser Glu Asp Gly His Gln Ser Leu Phe
 100 105 110

Gly Phe Leu Gly Ile Ser Tyr Leu Thr Phe Arg Ala Val Ala Met Ile
 115 120 125

Ile Glu Met Arg Asp Gly Val Leu Lys Glu Phe Thr Leu Trp Glu Phe
 130 135 140

Leu Arg Phe Leu Leu Phe Phe Pro Thr Phe Ser Ser Gly Pro Ile Asp
 145 150 155 160

Arg Phe Lys Arg Phe Asn Glu Asp Tyr Ile Asn Ile Pro Asp Arg Asn
 165 170 175

Glu Leu Leu Asp Met Leu Gly Gln Ala Ile His Tyr Leu Met Leu Gly
 180 185 190

Phe Leu Tyr Lys Phe Ile Leu Ala Tyr Ile Phe Gly Ser Leu Ile Met
 195 200 205

Pro Pro Leu Lys Glu Leu Ala Leu Glu Gln Gly Gly Val Phe Asn Trp
 210 215 220

Pro Thr Leu Gly Val Met Tyr Ala Phe Gly Phe Asp Leu Phe Phe Asp
 225 230 235 240

Phe Ala Gly Tyr Thr Met Phe Ala Leu Ala Ile Ser Asn Leu Met Gly
 245 250 255

Ile Lys Ser Pro Ile Asn Phe Asp Lys Pro Phe Lys Ser Arg Asp Leu
 260 265 270

Lys Glu Phe Trp Asn Arg Trp His Met Ser Leu Ser Phe Trp Phe Arg
 275 280 285

Asp Phe Val Phe Met Arg Leu Val Lys Leu Leu Val Lys Asn Lys Val
 290 295 300

Phe Lys Asn Arg Asn Val Thr Ser Ser Val Ala Tyr Ile Ile Asn Met
 305 310 315 320

Leu Leu Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Ala Tyr
 325 330 335

Gly Leu Phe His Gly Ile Gly Leu Val Ile Asn Asp Ala Trp Val Arg
 340 345 350

Lys Lys Lys Asn Xaa Asn Lys Glu Arg Arg Leu Ala Lys Lys Pro Leu
 355 360 365

Leu Pro Glu Asn Lys Trp Thr Tyr Ala Leu Gly Val Phe Ile Thr Phe
 370 375 380

Asn Val Val Met Phe Ser Phe Leu Ile Phe Ser Gly Phe Leu Asp Leu
 385 390 395 400

Leu Trp Phe Pro Gln Pro His Asn Lys
 405

<210> 32

<211> 100

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (99)

<223>

<400> 32

atg	aat	aaa	ata	acg	aca	tta	tca	acc	atc	gcc	ctg	act	tta	atg	ctt	48
Met	Asn	Lys	Ile	Thr	Thr	Leu	Ser	Thr	Ile	Ala	Leu	Thr	Leu	Met	Leu	
1				5					10					15		

tgc	gtt	gga	tgt	tct	gcc	aat	aaa	gat	aat	caa	aaa	act	aaa	act	gag	96
Cys	Val	Gly	Cys	Ser	Ala	Asn	Lys	Asp	Asn	Gln	Lys	Thr	Lys	Thr	Glu	
			20					25					30			

gat	c	100
Asp		

<210> 33

<211> 33

<212> PRT

<213> Streptococcus agalactiae

<400> 33

Met	Asn	Lys	Ile	Thr	Thr	Leu	Ser	Thr	Ile	Ala	Leu	Thr	Leu	Met	Leu
1				5					10					15	

Cys	Val	Gly	Cys	Ser	Ala	Asn	Lys	Asp	Asn	Gln	Lys	Thr	Lys	Thr	Glu
			20					25					30		

Asp

<210> 34

<211> 654

<212> DNA

<213> Streptococcus agalactiae

<220>

<221> CDS

<222> (1) .. (654)

<223>

<400> 34

gat	cga	ggc	tat	caa	gaa	gca	atg	gct	aaa	cta	agg	aaa	act	tac	ggc	48
Asp	Arg	Gly	Tyr	Gln	Glu	Ala	Met	Ala	Lys	Leu	Arg	Lys	Thr	Tyr	Gly	
1				5				10					15			

gaa	tat	ggg	tta	ggg	gtt	tct	aca	gga	tta	gat	tta	cct	gaa	tca	gaa	96
Glu	Tyr	Gly	Leu	Gly	Val	Ser	Thr	Gly	Leu	Asp	Leu	Pro	Glu	Ser	Glu	
			20					25					30			

ggg	tat	gta	cct	gga	aaa	tac	agc	tta	gga	aca	act	cta	atg	gaa	tcg	144
Gly	Tyr	Val	Pro	Gly	Lys	Tyr	Ser	Leu	Gly	Thr	Thr	Leu	Met	Glu	Ser	
		35					40					45				

ttc	ggg	cag	tat	gat	gcc	tat	aca	cca	atg	caa	ctt	ggg	cag	tat	atc	192
Phe	Gly	Gln	Tyr	Asp	Ala	Tyr	Thr	Pro	Met	Gln	Leu	Gly	Gln	Tyr	Ile	
	50					55					60					

tca	act	att	gcg	aat	aat	ggg	aat	cgt	tta	gca	cct	cac	gtg	gtt	tca	240
Ser	Thr	Ile	Ala	Asn	Asn	Gly	Asn	Arg	Leu	Ala	Pro	His	Val	Val	Ser	
65					70				75					80		

gat	atc	tat	gaa	ggg	aat	gat	tct	aat	aag	ttc	gct	caa	ttg	gtt	cgt	288
Asp	Ile	Tyr	Glu	Gly	Asn	Asp	Ser	Asn	Lys	Phe	Ala	Gln	Leu	Val	Arg	
			85					90					95			

tca	atc	act	cct	aaa	aca	cta	aat	aag	ata	gct	atc	tca	gat	caa	gag	336
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ser Ile Thr Pro Lys Thr Leu Asn Lys Ile Ala Ile Ser Asp Gln Glu
 100 105 110

tta gcc att att caa gaa ggt ttt tat aac gtt gtc aat agt gga agt 384
 Leu Ala Ile Ile Gln Glu Gly Phe Tyr Asn Val Val Asn Ser Gly Ser
 115 120 125

ggc tat gca act ggt acg tca atg agg ggg aat gtg aca acc att agy 432
 Gly Tyr Ala Thr Gly Thr Ser Met Arg Gly Asn Val Thr Thr Ile Ser
 130 135 140

ggc aaa act ggt acc gct gaa aca ttt gct aaa aat ata aat gga caa 480
 Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Ile Asn Gly Gln
 145 150 155 160

aca gtt tct acc tac aac tta aac gct att gcc tac gat act aat cgt 528
 Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp Thr Asn Arg
 165 170 175

aaa ata gca gta gcg gta atg tat ccg cat gtt aca act gat aca aca 576
 Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr Asp Thr Thr
 180 185 190

aaa tcc cat caa tta gtt gca cga gat atg att gat caa tat att tca 624
 Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln Tyr Ile Ser
 195 200 205

cag tca cag gac aat aag aga gga cat tga 654
 Gln Ser Gln Asp Asn Lys Arg Gly His
 210 215

<210> 35

<211> 217

<212> PRT

<213> Streptococcus agalactiae

<400> 35

Asp Arg Gly Tyr Gln Glu Ala Met Ala Lys Leu Arg Lys Thr Tyr Gly
 1 5 10 15

Glu Tyr Gly Leu Gly Val Ser Thr Gly Leu Asp Leu Pro Glu Ser Glu
 20 25 30

Gly Tyr Val Pro Gly Lys Tyr Ser Leu Gly Thr Thr Leu Met Glu Ser
 35 40 45

Phe Gly Gln Tyr Asp Ala Tyr Thr Pro Met Gln Leu Gly Gln Tyr Ile
 50 55 60

Ser Thr Ile Ala Asn Asn Gly Asn Arg Leu Ala Pro His Val Val Ser
 65 70 75 80

Asp Ile Tyr Glu Gly Asn Asp Ser Asn Lys Phe Ala Gln Leu Val Arg
 85 90 95

Ser Ile Thr Pro Lys Thr Leu Asn Lys Ile Ala Ile Ser Asp Gln Glu
 100 105 110

Leu Ala Ile Ile Gln Glu Gly Phe Tyr Asn Val Val Asn Ser Gly Ser
 115 120 125

Gly Tyr Ala Thr Gly Thr Ser Met Arg Gly Asn Val Thr Thr Ile Ser
 130 135 140

Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Ile Asn Gly Gln
 145 150 155 160

Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp Thr Asn Arg
 165 170 175

Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr Asp Thr Thr
 180 185 190

Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln Tyr Ile Ser
 195 200 205

Gln Ser Gln Asp Asn Lys Arg Gly His
 210 215